

## SEQUENCE LISTING

&lt;110&gt; Fox, Brian

Holloway, James L.

<120> ADIPOCYTE COMPLMENT RELATED PROTEIN  
ZACRP13

&lt;130&gt; 00-96

&lt;150&gt; US 60/253,924

&lt;151&gt; 2000-11-29

&lt;160&gt; 7

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 1381

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2).. (1381)

&lt;400&gt; 1

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gtt	gct	gga	cct	cca	gca	cac	ccc	agg	ccc	cca	gaa	gaa	gtg	ggg	cct	97
Val	Ala	Gly	Pro	Pro	Ala	His	Pro	Arg	Pro	Pro	Glu	Glu	Val	Gly	Pro	
			20					25						30		

cct	ggt	gca	cca	ggt	tta	cca	caa	tat	aca	gga	gaa	ata	agt	gaa	atg	145
Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gln	Tyr	Thr	Gly	Glu	Ile	Ser	Glu	Met	
			35					40						45		

aca	aaa	tgc	ccc	tgt	cct	gat	ata	gaa	agg	tca	gcc	ttt	act	gtg	aag	193
Thr	Lys	Cys	Pro	Cys	Pro	Asp	Ile	Glu	Arg	Ser	Ala	Phe	Thr	Val	Lys	
		50					55					60				

ctc agt gga aaa ctt cct ctt cct ttc aag ccc atc atc ttc aca ggg Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly 65 70 75 80	241
gtc ctg tac aat gcc cag agg gat tta aag gag gcc atg gga gtc ttt Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe 85 90 95	289
gct tgc agg gtg cct ggg aat tac tac tcc agc ttt gat gtt gag ctg Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu 100 105 110	337
cat cat tgc aag gtg aat att tgg cta atg agg aag caa att ttg gct His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala 115 120 125	385
aat aag gaa gaa att tct aag cag caa agc att caa gag gtg act tgg Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp 130 135 140	433
gtg ctg tta aag gca ttc agt ttc ata agg gag gca gag cat aag agt Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser 145 150 155 160	481
tca gaa aat ttg cac cct gac aat gtg ata aaa aag aaa aac cca ttt Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe 165 170 175	529
tct gag ggg aaa ttc aag ctg gct gca gaa att tgc ata tgt aat gag Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu 180 185 190	577
gag ctg aat gtt aat cct caa gac aat ggg gaa aat atc tcc tgg aca Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr 195 200 205	625
tgt cag agg tct tca cag cag tcc atc aaa tca ctg gcc tgg agg cct Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro 210 215 220	673
agg aga aaa tgg ttt tgt ggg aca ggc cca ggg tcc ctg tgc tgt gtg	721

Arg	Arg	Lys	Trp	Phe	Cys	Gly	Thr	Gly	Pro	Gly	Ser	Leu	Cys	Cys	Val	
225					230					235					240	
cag	cct	aga	gac	ttg	gtg	ccc	tgt	gtc	cca	ggt	aat	tca	gct	gtg	gct	769
Gln	Pro	Arg	Asp	Leu	Val	Pro	Cys	Val	Pro	Val	Asn	Ser	Ala	Val	Ala	
				245					250					255		
tca	gag	ggg	gca	agc	ccc	aag	cct	tgg	cag	ctt	cca	agt	ggg	gtt	gag	817
Ser	Glu	Gly	Ala	Ser	Pro	Lys	Pro	Trp	Gln	Leu	Pro	Ser	Gly	Val	Glu	
			260					265					270			
cct	gtg	ggg	gca	aag	aag	tca	aga	att	gag	gtt	tgg	gaa	cct	cca	atc	865
Pro	Val	Gly	Ala	Lys	Lys	Ser	Arg	Ile	Glu	Val	Trp	Glu	Pro	Pro	Ile	
			275				280					285				
aga	ttt	cag	aag	ata	tat	gga	aac	ccc	tgg	atg	ccc	agg	cag	aag	ttt	913
Arg	Phe	Gln	Lys	Ile	Tyr	Gly	Asn	Pro	Trp	Met	Pro	Arg	Gln	Lys	Phe	
	290					295					300					
gct	gta	ggg	gtg	ggg	tcc	tca	tgg	aga	acc	tct	gca	agg	gta	gta	caa	961
Ala	Val	Gly	Val	Gly	Ser	Ser	Trp	Arg	Thr	Ser	Ala	Arg	Val	Val	Gln	
305					310					315					320	
aag	gga	aat	gtt	ggg	tgg	gag	ccc	cca	cac	aga	gtc	ccc	agt	ggg	gct	1009
Lys	Gly	Asn	Val	Gly	Trp	Glu	Pro	Pro	His	Arg	Val	Pro	Ser	Gly	Ala	
				325					330					335		
cca	tct	agt	aga	gct	gtg	aga	aga	agt	cca	cca	tcc	tcc	aga	ctc	cag	1057
Pro	Ser	Ser	Arg	Ala	Val	Arg	Arg	Ser	Pro	Pro	Ser	Ser	Arg	Leu	Gln	
			340					345					350			
aag	ggg	aga	tcc	act	gac	agc	ttg	cag	cat	gtg	cct	gaa	aaa	tcc	aca	1105
Lys	Gly	Arg	Ser	Thr	Asp	Ser	Leu	Gln	His	Val	Pro	Glu	Lys	Ser	Thr	
		355					360					365				
gac	act	cag	tgc	cag	cct	gtg	aaa	gca	gca	ggg	atg	gag	tct	gta	ccc	1153
Asp	Thr	Gln	Cys	Gln	Pro	Val	Lys	Ala	Ala	Gly	Met	Glu	Ser	Val	Pro	
	370					375					380					
tac	aaa	acc	gta	gtg	gca	gag	ctg	acc	aag	acc	gtg	gga	atc	tac	ctc	1201
Tyr	Lys	Thr	Val	Val	Ala	Glu	Leu	Thr	Lys	Thr	Val	Gly	Ile	Tyr	Leu	
385					390					395					400	

ttg cat tgt cat gac ctg gac gtg aga cat gga gtc aaa aga gat cat 1249  
 Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His  
                   405                  410                  415

ttt gga gct tta aga ttt gac tgc ccc act gga ttt cgg act tat atg 1297  
 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met  
                   420                  425                  430

ggg ccc gta ccc ctt tgt ttt ggc caa ttt ttt cca ttt gga act gcc 1345  
 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala  
                   435                  440                  445

gta ttt acc caa tgc ctg tac ctc cat tgt atg tag 1381  
 Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met \*  
                   450                  455

<210> 2

<211> 459

<212> PRT

<213> Homo sapiens

<400> 2

Ile Val Val Ile Pro Val Leu Ile Thr Ala Val Ile Glu His Val Glu  
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 Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro  
                   20                  25                  30  
 Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met  
                   35                  40                  45  
 Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys  
                   50                  55                  60  
 Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly  
 65                  70                  75                  80  
 Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe  
                   85                  90                  95  
 Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu  
                   100                  105                  110  
 His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala  
                   115                  120                  125  
 Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp  
                   130                  135                  140  
 Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser  
 145                  150                  155                  160

Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe  
 165 170 175  
 Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu  
 180 185 190  
 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr  
 195 200 205  
 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro  
 210 215 220  
 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val  
 225 230 235 240  
 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala  
 245 250 255  
 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu  
 260 265 270  
 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile  
 275 280 285  
 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe  
 290 295 300  
 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln  
 305 310 315 320  
 Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala  
 325 330 335  
 Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln  
 340 345 350  
 Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr  
 355 360 365  
 Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro  
 370 375 380  
 Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu  
 385 390 395 400  
 Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His  
 405 410 415  
 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met  
 420 425 430  
 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala  
 435 440 445  
 Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met  
 450 455

&lt;210&gt; 3

&lt;211&gt; 1377

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Degenerate polynucleotide encoding a polypeptide  
of SEQ ID NO:2

<221> variation

<222> (1)...(1377)

<223> Each n is independently A, T, G, or C.

<221> misc\_feature

<222> (1)...(1377)

<223> n = A,T,C or G

<400> 3

athgtngtna	thcngtnyt	nathacngcn	gtathgarc	aygtngargt	ngcnggnccn	60	
ccngcncayc	cnmgncncnc	ngargargtn	ggncncncng	grgcncncng	nytnccncar	120	
tayacnggng	arathwsnga	ratgacnaar	tgyccntgyc	cngayathga	rmgnwsngcn	180	
ttyacngtna	arytnwsngg	naarytnccn	ytncnttya	arccnathat	httyacnggn	240	
gtnytntaya	aygcncarmg	ngayytnaar	gargcnatgg	gngtnttygc	ntgymngtn	300	
ccnggnaayt	aytaywsnws	nttygaygt	garytncayc	aytgyaargt	naayathtg	360	
ytnatgmgn	arcarathyt	ngcnaayaar	gargarathw	snaarcarca	rwsnathcar	420	
gargtnacnt	gggtnytnyt	naargcntty	wsnttyathm	gngargcnga	rcayaarwsn	480	
wsngaraaay	tncaayccnga	yaaygttnath	aaraaraara	ayccnttyws	ngarggnaar	540	
ttyaarytng	cngcngarat	htgyathtg	aaygargary	tnaaygtnaa	yccncargay	600	
aayggngara	ayathwsntg	gacntgyar	mgnwsnwsnc	arcarwsnat	haarwsnytn	660	
gcntggmgnc	cnmgnmgnaa	rtggtytg	ggnacnggnc	cnggnwsnyt	ntgytgygt	720	
carccnmng	ayytngtncc	ntgygtncn	gtnaaywsng	cngtngcnws	ngarggngcn	780	
wsnccnaarc	cntggcaryt	nccnwsnggn	gtngarccng	tnggngcnaa	raarwsnmgn	840	
athgargtnt	gggarccncc	nathmgntty	caraaratht	ayggnaaycc	ntggatgccn	900	
mgncaraart	tygcngtngg	ngtnggnwsn	wsntggmgna	cnwsngcnmg	ngtngtncar	960	
aarggnaayg	tnggntggga	rcnccncay	mgngtnccnw	snggngcncc	nwsnwsnmgn	1020	
gcngtnmgm	gnwsnccncc	nwsnwsnmgn	ytncaraarg	gnmgwnsnac	ngaywsnytn	1080	
carcaygtnc	cngaraarws	nacngayacn	cartgycarc	cngtnaargc	ngcnggnatg	1140	
garwsngtnc	cntayaarac	ngtngtngcn	garytnacna	aracngtngg	nathtayytn	1200	
ytncaytgyc	aygayytnga	ygtmgnca	ggngtnaarm	gngaycaytt	yggngcnnytn	1260	
mgnttygayt	gyccnacngg	nttymgna	cn	ngtncnnytn	ntgytgygt	1320	
carttyttyc	cnttyggna	ngcngtntty	acncartgyy	tn	ayyttnca	ytgyatg	1377

<210> 4

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Aromatic motif

<221> VARIANT

<222> (2)...(6)

<223> Each Xaa is any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan, or leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (26)...(26)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (28)...(31)

<223> Each Xaa is independently any amino acid residue

<400> 4

Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15			
Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa		
			20				25					30			

<210> 5  
 <211> 1731  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1731)

<400> 5

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Met	Leu	Ile	Glu	Ala	Tyr	Gly	Gly	Asp	Leu	Val	Ala	Gln	Gly	Ser	Lys	
1			5					10					15			

aaa	tgc	tgc	att	gga	gag	atg	ggg	tac	atg	cga	gtg	aca	atg	gga	aga	96
Lys	Cys	Cys	Ile	Gly	Glu	Met	Gly	Tyr	Met	Arg	Val	Thr	Met	Gly	Arg	
			20					25					30			

gtt	ggt	agc	tgg	aga	gaa	ctg	gga	aag	cct	tca	ggc	atc	tgg	gaa	atg	144
Val	Gly	Ser	Trp	Arg	Glu	Leu	Gly	Lys	Pro	Ser	Gly	Ile	Trp	Glu	Met	
			35					40					45			

gct	ggg	gat	aca	gag	gtg	aag	aag	aca	ggg	ttt	ctt	cag	gaa	ctc	act	192
Ala	Gly	Asp	Thr	Glu	Val	Lys	Lys	Thr	Gly	Phe	Leu	Gln	Glu	Leu	Thr	
			50					55					60			

ttc	cag	cag	gag	cct	ggc	atc	tcc	tcc	tct	cct	tct	tgc	tcc	cgc	tct	240
Phe	Gln	Gln	Glu	Pro	Gly	Ile	Ser	Ser	Ser	Pro	Ser	Cys	Ser	Arg	Ser	
			65				70				75				80	

tgc	cat	gtg	aca	cca	cct	gct	cca	cct	gca	tct	tct	gcc	ata	att	gta	288
Cys	His	Val	Thr	Pro	Pro	Ala	Pro	Pro	Ala	Ser	Ser	Ala	Ile	Ile	Val	
				85					90						95	

aga	ttc	ctg	agg	ccc	tca	cca	gaa	gca	gat	gcc	agc	agc	atg	ctt	att	336
Arg	Phe	Leu	Arg	Pro	Ser	Pro	Glu	Ala	Asp	Ala	Ser	Ser	Met	Leu	Ile	
				100					105					110		

gca	cag	tct	gta	gaa	ccg	ata	gtg	gtc	ata	cct	gtc	tta	ata	acg	gca	384
Ala	Gln	Ser	Val	Glu	Pro	Ile	Val	Val	Ile	Pro	Val	Leu	Ile	Thr	Ala	
			115					120						125		

gtc	att	gag	cat	gta	gaa	gtt	gct	gga	cct	cca	gca	cac	ccc	agg	ccc	432
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Val	Ile	Glu	His	Val	Glu	Val	Ala	Gly	Pro	Pro	Ala	His	Pro	Arg	Pro		
130						135					140						
cca	gaa	gaa	gtg	ggg	cct	cct	ggt	gca	cca	ggt	tta	cca	caa	tat	aca		480
Pro	Glu	Glu	Val	Gly	Pro	Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gln	Tyr	Thr		
145					150					155					160		
gga	gaa	ata	agt	gaa	atg	aca	aaa	tgc	ccc	tgt	cct	gat	ata	gaa	agg		528
Gly	Glu	Ile	Ser	Glu	Met	Thr	Lys	Cys	Pro	Cys	Pro	Asp	Ile	Glu	Arg		
				165					170					175			
tca	gcc	ttt	act	gtg	aag	ctc	agt	gga	aaa	ctt	cct	ctt	cct	ttc	aag		576
Ser	Ala	Phe	Thr	Val	Lys	Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys		
				180				185						190			
ccc	atc	atc	ttc	aca	ggg	gtc	ctg	tac	aat	gcc	cag	agg	gat	tta	aag		624
Pro	Ile	Ile	Phe	Thr	Gly	Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys		
		195					200					205					
gag	gcc	atg	gga	gtc	ttt	gct	tgc	agg	gtg	cct	ggg	aat	tac	tac	tcc		672
Glu	Ala	Met	Gly	Val	Phe	Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser		
	210					215					220						
agc	ttt	gat	gtt	gag	ctg	cat	cat	tgc	aag	gtg	aat	att	tgg	cta	atg		720
Ser	Phe	Asp	Val	Glu	Leu	His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met		
225					230					235					240		
agg	aag	caa	att	ttg	gct	aat	aag	gaa	gaa	att	tct	aag	cag	caa	agc		768
Arg	Lys	Gln	Ile	Leu	Ala	Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser		
				245					250					255			
att	caa	gag	gtg	act	tgg	gtg	ctg	tta	aag	gca	ttc	agt	ttc	ata	agg		816
Ile	Gln	Glu	Val	Thr	Trp	Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg		
			260					265					270				
gag	gca	gag	cat	aag	agt	tca	gaa	aat	ttg	cac	cct	gac	aat	gtg	ata		864
Glu	Ala	Glu	His	Lys	Ser	Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile		
		275					280					285					
aaa	aag	aaa	aac	cca	ttt	tct	gag	ggg	aaa	ttc	aag	ctg	gct	gca	gaa		912
Lys	Lys	Lys	Asn	Pro	Phe	Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu		
		290					295					300					

att tgc ata tgt aat gag gag ctg aat gtt aat cct caa gac aat ggg	960
Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly	
305 310 315 320	
gaa aat atc tcc tgg aca tgt cag agg tct tca cag cag tcc atc aaa	1008
Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys	
325 330 335	
tca ctg gcc tgg agg cct agg aga aaa tgg ttt tgt ggg aca ggc cca	1056
Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro	
340 345 350	
ggg tcc ctg tgc tgt gtg cag cct aga gac ttg gtg ccc tgt gtc cca	1104
Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro	
355 360 365	
gtt aat tca gct gtg gct tca gag ggt gca agc ccc aag cct tgg cag	1152
Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln	
370 375 380	
ctt cca agt ggt gtt gag cct gtg ggt gca aag aag tca aga att gag	1200
Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu	
385 390 395 400	
gtt tgg gaa cct cca atc aga ttt cag aag ata tat gga aac ccc tgg	1248
Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp	
405 410 415	
atg ccc agg cag aag ttt gct gta ggg gtg ggg tcc tca tgg aga acc	1296
Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr	
420 425 430	
tct gca agg gta gta caa aag gga aat gtt ggg tgg gag ccc cca cac	1344
Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His	
435 440 445	
aga gtc ccc agt ggg gct cca tct agt aga gct gtg aga aga agt cca	1392
Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro	
450 455 460	
cca tcc tcc aga ctc cag aag ggt aga tcc act gac agc ttg cag cat	1440

Pro	Ser	Ser	Arg	Leu	Gln	Lys	Gly	Arg	Ser	Thr	Asp	Ser	Leu	Gln	His	
465					470					475					480	
gtg	cct	gaa	aaa	tcc	aca	gac	act	cag	tgc	cag	cct	gtg	aaa	gca	gca	1488
Val	Pro	Glu	Lys	Ser	Thr	Asp	Thr	Gln	Cys	Gln	Pro	Val	Lys	Ala	Ala	
				485					490					495		
ggg	atg	gag	tct	gta	ccc	tac	aaa	acc	gta	gtg	gca	gag	ctg	acc	aag	1536
Gly	Met	Glu	Ser	Val	Pro	Tyr	Lys	Thr	Val	Val	Ala	Glu	Leu	Thr	Lys	
			500					505					510			
acc	gtg	gga	atc	tac	ctc	ttg	cat	tgt	cat	gac	ctg	gac	gtg	aga	cat	1584
Thr	Val	Gly	Ile	Tyr	Leu	Leu	His	Cys	His	Asp	Leu	Asp	Val	Arg	His	
		515					520					525				
gga	gtc	aaa	aga	gat	cat	ttt	gga	gct	tta	aga	ttt	gac	tgc	ccc	act	1632
Gly	Val	Lys	Arg	Asp	His	Phe	Gly	Ala	Leu	Arg	Phe	Asp	Cys	Pro	Thr	
	530					535					540					
gga	ttt	cgg	act	tat	atg	ggg	ccc	gta	ccc	ctt	tgt	ttt	ggc	caa	ttt	1680
Gly	Phe	Arg	Thr	Tyr	Met	Gly	Pro	Val	Pro	Leu	Cys	Phe	Gly	Gln	Phe	
545					550					555					560	
ttt	cca	ttt	gga	act	gcc	gta	ttt	acc	caa	tgc	ctg	tac	ctc	cat	tgt	1728
Phe	Pro	Phe	Gly	Thr	Ala	Val	Phe	Thr	Gln	Cys	Leu	Tyr	Leu	His	Cys	
			565					570						575		
atg																1731
Met																

&lt;210&gt; 6

&lt;211&gt; 577

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

Met	Leu	Ile	Glu	Ala	Tyr	Gly	Gly	Asp	Leu	Val	Ala	Gln	Gly	Ser	Lys	
1				5				10					15			
Lys	Cys	Cys	Ile	Gly	Glu	Met	Gly	Tyr	Met	Arg	Val	Thr	Met	Gly	Arg	
			20					25					30			

Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met  
 35 40 45  
 Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr  
 50 55 60  
 Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser  
 65 70 75 80  
 Cys His Val Thr Pro Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val  
 85 90 95  
 Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile  
 100 105 110  
 Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala  
 115 120 125  
 Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro  
 130 135 140  
 Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr  
 145 150 155 160  
 Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg  
 165 170 175  
 Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys  
 180 185 190  
 Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys  
 195 200 205  
 Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser  
 210 215 220  
 Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met  
 225 230 235 240  
 Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser  
 245 250 255  
 Ile Gln Glu Val Thr Trp Val Leu Leu Lys Ala Phe Ser Phe Ile Arg  
 260 265 270  
 Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile  
 275 280 285  
 Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu  
 290 295 300  
 Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly  
 305 310 315 320  
 Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys  
 325 330 335  
 Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro  
 340 345 350  
 Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro  
 355 360 365

Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln  
 370 375 380  
 Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu  
 385 390 395 400  
 Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp  
 405 410 415  
 Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr  
 420 425 430  
 Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His  
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 Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro  
 450 455 460  
 Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His  
 465 470 475 480  
 Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala  
 485 490 495  
 Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys  
 500 505 510  
 Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His  
 515 520 525  
 Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr  
 530 535 540  
 Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe  
 545 550 555 560  
 Phe Pro Phe Gly Thr Ala Val Phe Thr Gln Cys Leu Tyr Leu His Cys  
 565 570 575  
 Met

<210> 7

<211> 1731

<212> DNA

<213> Artificial Sequence

<220>

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of SEQ ID NO:6

<221> misc\_feature

<222> (1)...(1731)

<223> n = A,T,C or G

<400> 7

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aarccnwsng	gnathtgga	ratggcnggn	gayacngarg	tnaaraarac	nggnttyytn	180
cargarytna	cnttycarca	rgarccnggn	athwsnwsnw	snccnwsntg	ywsnmgnwsn	240
tgycaygtna	cncncncngc	nccncncngc	wsnwsngcna	thathgtnm	nttyytnmgn	300
ccnwsnccng	argcngaygc	nwsnwsnatg	ytnathgcnc	arwsngtnga	rccnathgtn	360
gtnathccng	tnytnathac	ngcngtnath	garcaytng	argtngcngg	nccncncngc	420
cayccnmgn	cncngarga	rgtnggnccn	ccngngcnc	cnggnytncc	ncartayacn	480
ggngarathw	sngaratgac	naartgyccn	tgycngaya	thgarmgnws	ngcnttyacn	540
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aaytaytayw	snwsnttyga	ygtngarytn	caycaytgya	argtnaayat	htggytnatg	720
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garaayathw	sntggacntg	ycarmgnwsn	wsncarcarw	snathaarws	nytngcntgg	1020
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aarttygcng	tnggngtngg	nwsnwsntgg	mgnaacnwsng	cnmgngtngt	ncaraarggn	1320
aaygtnggnt	gggarccnc	ncaymgngtn	ccnwsnggng	cncnwsnws	nmngcngtn	1380
mgnmgnwsnc	cncnwsnws	nmgnytnear	aargnmgnw	snacngayws	nytnearcay	1440
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gtncntaya	aracngtngt	ngcngarytn	acnaaracng	tnggnathta	yytnytnca	1560
tgycaygayy	tngaygtng	ncayggngtn	aarmnggayc	ayttyggngc	nytnmgntty	1620
gaytgyccna	cnggnttymg	nacntayatg	ggncngtnc	cnytnhtgyt	yggncartty	1680
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